

Sample: SRR6856085

FASTQ Quality

Filename	SRR6856085_R1.fastq.gz	SRR6856085_R2.fastq.gz
File Size	119.2 MB	148.2 MB
Q30 Passing	83.7%	61.79%
Mean Read Score	27.1	20.5
Average Read Length	266.7	266.7

Read Mapping against SRR6856085

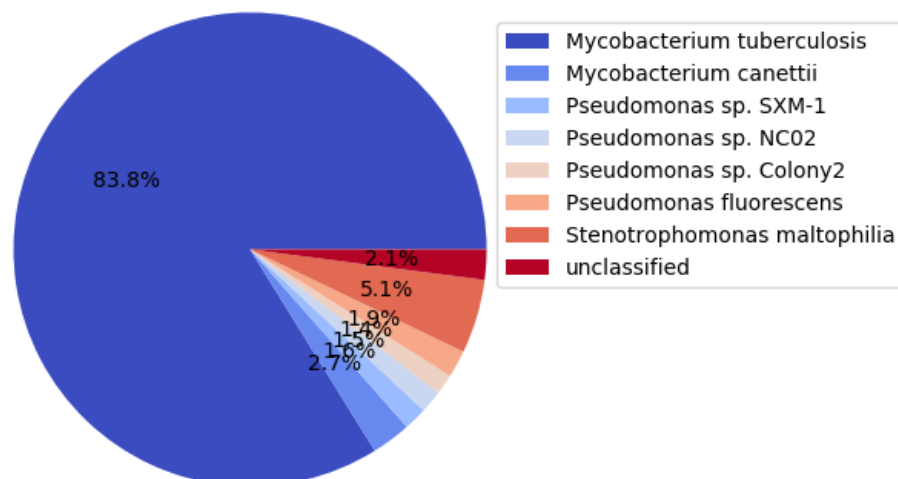
Mapped Paired Reads	Mapped Single Reads	Unmapped Reads	Unmapped Percent	Unmapped Assembled Contigs	
709,843	10,520	34,466	4.6%	assembly not done	
Duplicate Paired Reads	Duplicate Single Reads	Duplicate Percent of Mapped Reads			
1,006	3,863	0.4%			
BAM File	Reference Length	Genome with Coverage	Average Depth	No Coverage Bases	Quality SNPs
SRR6856085_nodup.bam	13,224,031	99.91%	28.0X	11,429	198

Assembly

Contig count	Contig length counts < 301-999bp >	Longest contig	Total length	N50	FASTQ calculated mean coverage
8,255	33 4,779 3,443	205,144	13,224,031	2,059	29.5X

FASTQ Identifications

FASTQ Read Identification



Identified using: Kraken and Bracken

Genome Size Comparisons

Mycobacterium tuberculosis	expected: 4,075,000 nt
SRR6856085	assembled: 13,224,031 nt

Sourmash Sequence Similarity

Similarity	ID
33.5%	KK317180.1 Mycobacterium tuberculosis TKK_05MA_0010 genomic scaffold adWtf-supercont1.1, whole genome shotgun sequence
33.5%	KK355761.1 Mycobacterium tuberculosis TB_RSA195 genomic scaffold adPkg-supercont1.1, whole genome shotgun sequence
33.5%	CPZO01000001.1 Mycobacterium tuberculosis genome assembly 7414_610, scaffold ERS075351SCcontig000001, whole genome shotgun sequence
33.5%	KK318777.1 Mycobacterium tuberculosis TKK_05SA_0010 genomic scaffold adWtG-supercont1.1, whole genome shotgun sequence
33.5%	KK351777.1 Mycobacterium tuberculosis TKK_02_0077 genomic scaffold adrPf-supercont1.1, whole genome shotgun sequence
33.5%	KK316877.1 Mycobacterium tuberculosis TKK_03_0106 genomic scaffold adYGX-supercont1.1, whole genome shotgun sequence
33.5%	KK316601.1 Mycobacterium tuberculosis TKK_03_0024 genomic scaffold adYGG-supercont1.1, whole genome shotgun sequence
33.5%	KK316595.1 Mycobacterium tuberculosis TKK_03_0023 genomic scaffold adYHJ-supercont1.1, whole genome shotgun sequence
33.5%	KK319462.1 Mycobacterium tuberculosis TKK_05SA_0025 genomic scaffold adWva-supercont1.1, whole genome shotgun sequence
33.5%	KK328467.1 Mycobacterium tuberculosis TKK-01-0077 genomic scaffold adbAV-supercont1.1, whole genome shotgun sequence

MLST 2.19.0

Schema-Sequence type: **mycobacteria-215**

MLST Detail: S14Z(17), L35(15), S19(20), L19(19), S12(20), S8(18), L16(22), S7(19)

Results provided by: MLST

AMRFinderPlus - version 3.11.2, database 2021-03-01.1

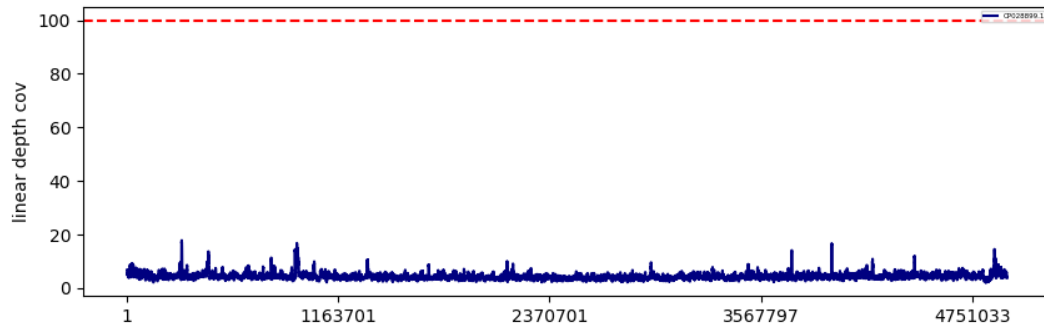
AMRFinderPlus Organism Option Not Found: Mycobacterium tuberculosis

Contig ID	Element	Gene	Description	% Cov	% Similar
NODE_109_length_5470_cov_2.062512	HEAT	shsP	small heat shock protein sHSP20-GI	55.92%	96.47%
NODE_109_length_5470_cov_2.062512	HEAT	yfdX1	heat resistance protein YfdX1	100.0%	90.79%
NODE_109_length_5470_cov_2.062512	HEAT	yfdX2	heat resistance protein YfdX2	100.0%	92.2%
NODE_109_length_5470_cov_2.062512	HEAT	hdeD-GI	heat resistance membrane protein HdeD-GI	100.0%	90.15%
NODE_109_length_5470_cov_2.062512	HEAT	trxLHR	heat resistance system thioredoxin Trx-GI	100.0%	94.52%
NODE_2129_length_1373_cov_3.493579	HEAT	psi-GI	heat resistance protein PsiE-GI	100.0%	97.58%
NODE_2129_length_1373_cov_3.493579	HEAT	kefB-GI	heat resistance system K+/H+ antiporter KefB-GI	50.96%	98.63%
NODE_31_length_51550_cov_39.310445	AMR	aac(2')-Ic	aminoglycoside N-acetyltransferase AAC(2')-Ic	100.0%	100.0%
NODE_3788_length_926_cov_2.065081	AMR	blaL1	L1 family subclass B3 metallo-beta-lactamase	68.86%	98.49%
NODE_50_length_28963_cov_46.123942	AMR	erm(37)	23S rRNA (adenine(2058)-N(6))-methyltransferase Erm(37)	100.0%	100.0%
NODE_52_length_28477_cov_41.048148	AMR	blaC	class A beta-lactamase BlaC	100.0%	100.0%
NODE_5893_length_603_cov_2.157563	AMR	emrA	multidrug efflux MFS transporter periplasmic adaptor subunit EmrA	51.15%	99.5%

Results provided by: AMRFinderPlus

Coverage Graph

SRR6856085 reads aligned against CP028899



ID	Average Depth	Genome Coverage	Genome Length	Ambiguous SNPs
CP028899.1	3.8X	84.2%	4,943,426	3,701

ID Detail

CP028899.1 *Stenotrophomonas maltophilia* strain AB550 chromosome, complete genome

BLAST nt - Assembly Identification

Nucleotide Representa- tion	Description
3,166,124	CP028899 <i>Stenotrophomonas maltophilia</i> strain AB550 chromosome, complete genome
1,515,570	CP038001 <i>Pseudomonas</i> sp. SXM-1 chromosome, complete genome
1,320,126	CP041820 <i>Mycobacterium tuberculosis</i> strain 4-0073P6C4 chromosome, complete genome
1,264,772	CP025624 <i>Pseudomonas</i> sp. NC02 chromosome, complete genome
1,225,238	CP000717 <i>Mycobacterium tuberculosis</i> F11, complete genome
1,161,774	CP065593 <i>Pseudomonas fluorescens</i> BBc6R8 chromosome
908,251	CP080030 <i>Pseudomonas</i> sp. Colony2 chromosome
205,144	CP002883 <i>Mycobacterium tuberculosis</i> BT1, complete genome
164,708	CP072790 <i>Mycobacterium tuberculosis</i> strain I0003447-5 chromosome, complete genome
159,644	CP025606 <i>Mycobacterium tuberculosis</i> strain GG-137-10 chromosome, complete genome
149,231	CP089610 <i>Mycobacterium tuberculosis</i> strain I0004290-8 chromosome, complete genome
140,286	CP053092 <i>Mycobacterium tuberculosis</i> strain 4860 chromosome, complete genome
129,654	CP028428 <i>Mycobacterium tuberculosis</i> strain CAS chromosome
111,587	CP069071 <i>Mycobacterium tuberculosis</i> strain N0136 chromosome, complete genome
102,253	CP054013 <i>Mycobacterium tuberculosis</i> strain FDAARGOS_757 chromosome, complete genome
90,483	CP025608 <i>Mycobacterium tuberculosis</i> strain GG-229-10 chromosome, complete genome
71,606	CP025605 <i>Mycobacterium tuberculosis</i> strain GG-134-11 chromosome, complete genome
70,861	CP039850 <i>Mycobacterium tuberculosis</i> variant bovis strain Danish 1331 chromosome, complete genome
67,809	CP040434 <i>Stenotrophomonas maltophilia</i> strain PEG-68 chromosome, complete genome
64,753	CP089779 <i>Mycobacterium tuberculosis</i> strain 01-R1134 chromosome, complete genome
45,582	CP025602 <i>Mycobacterium tuberculosis</i> strain GG-109-10 chromosome, complete genome
44,567	CP119371 <i>Pseudomonas</i> sp. CBSPCAW29 chromosome, complete genome
41,558	CP041812 <i>Mycobacterium tuberculosis</i> strain SEA07020250P6C4 chromosome, complete genome
40,842	LR134324 <i>Stenotrophomonas maltophilia</i> strain NCTC10259 genome assembly, chromosome: 1
37,680	CP012400 <i>Pseudomonas yamanorum</i> strain LBUM636 chromosome, complete genome
33,313	CP085551 <i>Mycobacterium tuberculosis</i> strain 405/2018 chromosome
32,933	CP020381 <i>Mycobacterium tuberculosis</i> strain MTB1 chromosome, complete genome
27,770	CP041816 <i>Mycobacterium tuberculosis</i> strain SEA00042P6C4 chromosome, complete genome
27,386	CP054014 <i>Mycobacterium tuberculosis</i> strain FDAARGOS_756 chromosome, complete genome
25,223	CP031058 <i>Stenotrophomonas maltophilia</i> strain SM 866 chromosome, complete genome
23,519	CP029773 <i>Stenotrophomonas maltophilia</i> strain SJTL3 chromosome, complete genome
21,292	CP130807 <i>Mycobacterium tuberculosis</i> strain MTb-Oman-3211392 chromosome, complete genome
19,732	CP052860 <i>Pseudomonas</i> sp. ADAK13 chromosome, complete genome
18,262	CP047258 <i>Mycobacterium tuberculosis</i> strain TCDC3 chromosome
17,124	CP001662 <i>Mycobacterium tuberculosis</i> KZN 4207, complete genome
17,123	CP130764 <i>Mycobacterium tuberculosis</i> strain MTb-Oman-3214760 chromosome, complete genome
16,423	CP019612 <i>Mycobacterium tuberculosis</i> strain H107 chromosome, complete genome
15,729	LT629793 <i>Pseudomonas yamanorum</i> strain LMG 27247 genome assembly, chromosome: 1
14,119	CP052856 <i>Pseudomonas</i> sp. ADAK22 chromosome, complete genome
11,286	CP010902 <i>Moraxella catarrhalis</i> strain MC8 chromosome
11,217	AP024684 <i>Stenotrophomonas pavanii</i> Y DNA, complete genome
11,205	HE798556 <i>Stenotrophomonas maltophilia</i> D457 complete genome
10,621	LS483372 <i>Pseudomonas fluorescens</i> strain NCTC10038 genome assembly, chromosome: 1
10,242	CP110972 <i>Pseudomonas poae</i> strain 5BF chromosome
9,900	CP050062 <i>Stenotrophomonas rhizophila</i> strain JC1 chromosome, complete genome
9,073	CP025600 <i>Mycobacterium tuberculosis</i> strain GG-77-11 chromosome, complete genome
8,924	CP054868 <i>Pseudomonas chlororaphis</i> strain PCLAR04 chromosome, complete genome
8,581	CP130774 <i>Mycobacterium tuberculosis</i> strain MTb-Oman-3214168 chromosome, complete genome
8,511	CP034537 <i>Pseudomonas poae</i> strain CAP-2018 chromosome, complete genome
8,317	CP099643 <i>Pseudomonas proteolytica</i> strain H160204 chromosome, complete genome
7,439	CP128404 <i>Stenotrophomonas</i> sp. 8(2023) chromosome, complete genome
7,273	CP077082 <i>Pseudomonas</i> sp. OE 28.3 chromosome, complete genome
6,737	CP067993 <i>Stenotrophomonas maltophilia</i> strain DHHJ chromosome, complete genome
6,009	CP119368 <i>Pseudomonas</i> sp. CBSPCGW29 chromosome, complete genome

Results provided by: BLAST nt database

BLAST nt - Assembly Identification - continued

Nucleotide Representa- tion	Description
5,785	CP130817 Mycobacterium tuberculosis strain MTb-Oman-32193 chromosome, complete genome
5,778	CP061011 Stenotrophomonas pavanii strain PI-27 chromosome
5,660	CP085559 Mycobacterium tuberculosis strain 416/2018 chromosome
4,845	CP049956 Stenotrophomonas maltophilia strain NCTC10498 chromosome, complete genome
4,789	CP010901 Moraxella catarrhalis strain MC6 chromosome
4,544	CP023269 Pseudomonas sp. MYb193 chromosome, complete genome
4,411	CP117436 Pseudomonas sp. FP2338 chromosome, complete genome
4,387	CP025603 Mycobacterium tuberculosis strain GG-121-10 chromosome, complete genome
4,334	CP122540 Pseudomonas brenneri strain K5-sn1400 chromosome, complete genome
4,253	CP060022 Stenotrophomonas maltophilia strain UHH_PC240 chromosome
4,222	CP081943 Pseudomonas sp. MM213 chromosome, complete genome
4,205	CP020369 Pseudomonas tolaasii strain 2192T chromosome
4,137	CP034492 Eukaryotic synthetic construct chromosome 14
3,862	CP034496 Eukaryotic synthetic construct chromosome 18
3,855	CP034425 Pseudomonas libanensis strain DMSP-1 chromosome, complete genome
3,667	CP119369 Pseudomonas sp. CBSPAW29 chromosome, complete genome
3,663	CP060023 Stenotrophomonas maltophilia strain UHH_PC239 chromosome
3,588	CP117464 Pseudomonas lurida strain FP1465 chromosome, complete genome
3,465	OX460939 Pseudomonas fluorescens strain SF1671 genome assembly, chromosome: SF1671_c1
3,349	LT703009 Andersenella sp. Alg231_50 genome assembly, chromosome: VII
3,342	CP101125 Pseudomonas nunensis strain In5 chromosome, complete genome
3,161	CP117438 Pseudomonas fluorescens strain FP2327 chromosome, complete genome
3,141	CP117448 Pseudomonas simiae strain FP2084 chromosome, complete genome
3,073	CP031167 Stenotrophomonas sp. ASS1 chromosome, complete genome
3,060	LT906480 Stenotrophomonas maltophilia strain NCTC10257 genome assembly, chromosome: 1
3,037	CP010573 Moraxella catarrhalis strain MC1 chromosome
3,034	CP027405 Moraxella catarrhalis strain FDAARGOS_304 chromosome, complete genome
3,021	CP101622 Stenotrophomonas maltophilia strain CYZ chromosome, complete genome
3,012	CP069594 Pseudomonas sp. Y39-6 chromosome, complete genome
2,910	CP027754 Pseudomonas synxantha strain 30B chromosome, complete genome
2,816	CP104323 Stenotrophomonas maltophilia strain ACYCc.3B chromosome, complete genome
2,692	CP087196 Pseudomonas sp. B21-015 chromosome, complete genome
2,617	CP119772 Pseudomonas sp. D3 chromosome, complete genome
2,586	LT629706 Pseudomonas poae strain BS2776 genome assembly, chromosome: I
2,582	CP097092 MAG: Lancefieldella parvula isolate JCVI-JB-Lp32 chromosome, complete genome
2,519	CP088244 Stenotrophomonas maltophilia strain 2013-SM4 chromosome, complete genome
2,499	CP129402 Pseudomonas veronii strain OST1911 chromosome, complete genome
2,479	CP102929 Pseudomonas sp. CBS chromosome, complete genome
2,472	CP025780 Stenotrophomonas sp. Pemsol chromosome
2,415	BK028718 MAG TPA_asm: Caudoviricetes sp. isolate ctQcn1, partial genome
2,415	CP010900 Moraxella catarrhalis strain MC5 chromosome
2,285	CP114115 Pseudomonas sp. GXZC chromosome, complete genome
2,253	CP119367 Pseudomonas sp. CBSPGW29 chromosome, complete genome
2,206	CP089551 Pseudomonas sp. 7-41 chromosome, complete genome
2,143	CP043578 Stenotrophomonas maltophilia strain T50-20 chromosome, complete genome
2,098	LS483445 Moraxella catarrhalis strain NCTC11020 genome assembly, chromosome: 1
2,092	CP133413 Stenotrophomonas maltophilia strain BF-25-0308-St chromosome
2,073	NC_074659 Pseudomonas phage phiAH14a, complete genome
2,055	CP019856 Pseudomonas azotoformans strain F77, complete genome
2,011	LR722623 Hordeum vulgare subsp. vulgare genome assembly, chromosome: 0H
1,986	CP027743 Pseudomonas chlororaphis subsp. aurantiaca strain CW2 chromosome, complete genome
1,932	CP034662 Moraxella catarrhalis strain 46P58B1 chromosome, complete genome
1,900	CP048408 Pseudomonas fluorescens strain DR397 chromosome, complete genome
1,897	CP068261 Homo sapiens isolate CHM13 chromosome 17

Results provided by: BLAST nt database

BLAST nt - Assembly Identification - continued

Nucleotide Representa- tion	Description
1,879	CP021768 <i>Stenotrophomonas</i> sp. WZN-1, complete genome
1,838	BK016437 MAG TPA_asm: <i>Caudoviricetes</i> sp. isolate ctiPh1, partial genome
1,817	CP034338 <i>Pseudomonas</i> <i>oryziphila</i> strain 1257 chromosome, complete genome
1,813	CP094975 <i>Pseudomonas</i> sp. PIA16 chromosome, complete genome
1,812	BK017244 MAG TPA_asm: <i>Caudoviricetes</i> sp. isolate ct0cU1, partial genome
1,787	CP034495 Eukaryotic synthetic construct chromosome 17
1,767	CP029983 <i>Pseudomonas</i> sp. LG1E9 chromosome, complete genome
1,755	CP090423 <i>Stenotrophomonas</i> <i>maltophilia</i> strain GYH chromosome, complete genome
1,735	LT629699 <i>Pseudomonas</i> <i>libanensis</i> strain BS2975 genome assembly, chromosome: I
1,680	CP119382 <i>Pseudomonas</i> <i>kermanshahensis</i> strain Mr36 chromosome, complete genome
1,669	CP117444 <i>Pseudomonas</i> sp. FP2254 chromosome, complete genome
1,637	CP117462 <i>Pseudomonas</i> <i>rhodesiae</i> strain FP1707 chromosome, complete genome
1,627	CP011507 <i>Pseudomonas</i> <i>trivialis</i> strain IHBB745, complete genome
1,601	CP068258 <i>Homo sapiens</i> isolate CHM13 chromosome 20
1,545	LT963391 <i>Pseudomonas</i> <i>syringae</i> pv. <i>cerasicola</i> isolate CFBP6109 genome assembly, chromosome: 1
1,537	CP040431 <i>Stenotrophomonas</i> <i>maltophilia</i> strain sm454 chromosome, complete genome
1,501	CP034516 Eukaryotic synthetic construct chromosome 13
1,494	CP015639 <i>Pseudomonas</i> <i>lurida</i> strain L228 chromosome, complete genome
1,486	CP071128 <i>Mycobacterium</i> <i>tuberculosis</i> strain 267/47W148 chromosome, complete genome
1,481	LT629972 <i>Pseudomonas</i> <i>fuscovaginae</i> strain LMG 2158 genome assembly, chromosome: I
1,469	CP034493 Eukaryotic synthetic construct chromosome 15
1,465	CP002986 <i>Stenotrophomonas</i> <i>maltophilia</i> JV3, complete genome
1,465	CP080090 <i>Pseudomonas</i> sp. YeP6b chromosome, complete genome
1,465	AP021904 <i>Pseudomonas</i> sp. Ost2 DNA, complete genome
1,454	BK024360 MAG TPA_asm: <i>Caudoviricetes</i> sp. isolate ctpqn2, partial genome
1,416	CP086206 <i>Pseudomonas</i> sp. HN8-3 chromosome, complete genome
1,404	MH043576 <i>Homo sapiens</i> isolate CAR256 mitochondrion, complete genome
1,400	CP034494 Eukaryotic synthetic construct chromosome 16
1,385	CP092411 <i>Pseudomonas</i> <i>palleroniana</i> strain Q1 chromosome, complete genome
1,382	CP068256 <i>Homo sapiens</i> isolate CHM13 chromosome 22
1,372	CP006668 <i>Ralstonia</i> <i>pickettii</i> DTP0602 chromosome 2, complete sequence
1,367	CP034499 Eukaryotic synthetic construct chromosome 20
1,347	CP034501 Eukaryotic synthetic construct chromosome 22
1,343	CP077083 <i>Pseudomonas</i> <i>salmasensis</i> strain SWRI126 chromosome, complete genome
1,280	CP117456 <i>Pseudomonas</i> <i>simiae</i> strain FP1885 chromosome, complete genome
1,273	CP003880 <i>Pseudomonas</i> sp. UW4, complete genome
1,221	CP110885 <i>Pseudomonas</i> <i>lurida</i> strain CFBP13722 chromosome
1,217	CP068262 <i>Homo sapiens</i> isolate CHM13 chromosome 16
1,212	CP104408 <i>Pseudomonas</i> <i>fluorescens</i> strain Ant01 chromosome, complete genome
1,209	CP034665 <i>Moraxella</i> <i>catarrhalis</i> strain 142P87B1 chromosome, complete genome
1,199	AC233976 <i>Homo sapiens</i> BAC clone RP11-486N10 from chromosome x, complete sequence
1,190	CP027740 <i>Pseudomonas</i> <i>chlororaphis</i> subsp. <i>piscium</i> strain ChPhzS140 chromosome, complete genome
1,183	CP031450 <i>Pseudomonas</i> <i>fluorescens</i> strain SIK_W1 chromosome, complete genome
1,180	LS483377 <i>Stenotrophomonas</i> <i>maltophilia</i> strain NCTC10258 genome assembly, chromosome: 1
1,179	AP022213 <i>Pseudomonas</i> <i>otitidis</i> DNA, complete genome, strain: WP8-S17-CRE-03
1,150	CP027727 <i>Pseudomonas</i> sp. R5-89-07 chromosome, complete genome
1,150	CP037901 <i>Cupriavidus</i> <i>metallidurans</i> strain BS1 chromosome c2, complete sequence
1,147	AC061958 <i>Homo sapiens</i> chromosome 3 clone RP11-6B7, complete sequence
1,132	CP087173 <i>Pseudomonas</i> <i>donghuensis</i> strain B21-043 chromosome, complete genome
1,130	BK023740 MAG TPA_asm: <i>Caudoviricetes</i> sp. isolate ctiT52, partial genome
1,129	CP040435 <i>Stenotrophomonas</i> <i>maltophilia</i> strain PEG-42 chromosome, complete genome
1,110	CP041753 <i>Pseudomonas</i> sp. ATCC 43928 chromosome, complete genome
1,103	CP052862 <i>Pseudomonas</i> sp. ADAK2 chromosome, complete genome
1,094	CP080330 <i>Pseudomonas</i> sp. ArH3a chromosome, complete genome

Results provided by: BLAST nt database

BLAST nt - Assembly Identification - continued

Nucleotide Representation	Description
1,078	CP048114 Edaphobacter sp. 12200R-103 chromosome, complete genome
1,059	CP003122 Streptococcus parasanguinis FW213, complete genome
1,044	AC104843 Homo sapiens BAC clone RP11-1246H4 from 7, complete sequence
1,043	CP014060 Achromobacter xylosoxidans strain FDAARGOS_147 chromosome, complete genome
1,030	LT629762 Pseudomonas prosekii strain LMG 26867 genome assembly, chromosome: I
1,028	LR739071 Pseudomonas aeruginosa strain C7-25 genome assembly, chromosome: C7-25
1,021	AP024903 Vibrio rhizosphaerae LMG 23790 DNA, chromosome 1, complete sequence
1,015	BK052033 MAG TPA_asm: Caudoviricetes sp. isolate cta892, partial genome
1,014	CP066169 Pseudomonas simiae strain K-Hf-L9 chromosome, complete genome
1,010	CP014546 Pseudomonas azotoformans strain S4 chromosome, complete genome
1,009	CP034666 Moraxella catarrhalis strain 5P47B2 chromosome, complete genome
992	CP027756 Pseudomonas synxantha strain R6-28-08 chromosome, complete genome
987	CP031477 Haemophilus parainfluenzae strain M27794 chromosome, complete genome
986	CP011525 Pseudomonas sp. JY-Q, complete genome
983	CP034522 Eukaryotic synthetic construct chromosome 19
977	CP081946 Pseudomonas sp. DR48 chromosome, complete genome
972	CP068260 Homo sapiens isolate CHM13 chromosome 18
972	CP081178 Pseudomonas mandelii strain KGI_MA19 chromosome, complete genome
971	CP077079 Pseudomonas asgharzadehiana strain SWRI132 chromosome, complete genome
967	CP063194 Corynebacterium jeikeium strain DSM 45997 chromosome, complete genome
967	CP014065 Achromobacter xylosoxidans strain FDAARGOS_162 chromosome, complete genome
961	CP117424 Pseudomonas sp. FP833 chromosome, complete genome
958	CP034500 Eukaryotic synthetic construct chromosome 21
958	CP034497 Eukaryotic synthetic construct chromosome 19
956	CP113949 Pseudomonas sp. BSw22131 chromosome, complete genome
954	CP027723 Pseudomonas orientalis strain 8B chromosome, complete genome
949	LS483371 Paucimonas lemoignei strain NCTC10937 genome assembly, chromosome: 1
932	AP023477 Homo sapiens DNA, chromosome 17, nearly complete genome
930	CP018059 Moraxella catarrhalis strain CCRI-195ME chromosome, complete genome
926	XM_008330486 PREDICTED: Cynoglossus semilaevis SR-related CTD associated factor 1 (scaf1), mRNA
921	AL662896 Human DNA sequence from clone RP13-218H24 on chromosome X, complete sequence
920	CP027725 Pseudomonas orientalis strain R2-66-08W chromosome, complete genome
912	CP049820 Streptococcus sp. ZB199 chromosome, complete genome
907	AC090938 Homo sapiens chromosome 3 clone RP11-101A4 map 3p, complete sequence
906	CP032618 Pseudomonas fluorescens strain PF08 chromosome, complete genome
888	CP045302 Azotobacter salinisolans strain KACC 13899 chromosome, complete genome
888	CP117435 Pseudomonas sp. FP453 chromosome, complete genome
877	CP068263 Homo sapiens isolate CHM13 chromosome 15
872	CP019398 Pseudomonas sp. S34 chromosome, complete genome
828	CP130043 Pseudomonas kielensis strain ZE23JCe16 chromosome, complete genome
813	CP049044 Pseudomonas psychrophila strain KM02 chromosome, complete genome
810	CP080494 Pseudomonas sp. So3.2b chromosome, complete genome
803	CP076114 Pseudomonas seleniipraecipitans strain D1-6 chromosome, complete genome
798	CP058636 Pseudomonas sp. DS1 chromosome, complete genome
790	CP070980 Pseudomonas rhodesiae strain AAMF24 chromosome, complete genome
781	CP034510 Eukaryotic synthetic construct chromosome Y
780	CP087176 Pseudomonas sp. B21-040 chromosome, complete genome
765	AP022577 Mycolicibacterium aubagnense JCM 15296 DNA, complete genome
760	AP023835 Homo sapiens DNA, sequence_id: unplaced_0350
760	AL360084 Human DNA sequence from clone RP11-124M17 on chromosome 9, complete sequence
758	CP007637 Pseudomonas simiae strain WCS417 genome
757	AC000159 Homo sapiens Chromosome 11q13 BAC Clone b79g17, complete sequence
756	NG_011605 Homo sapiens OPA1 mitochondrial dynamin like GTPase (OPA1), RefSeqGene (LRG_337) on chro
750	AP021867 Stenotrophomonas maltophilia KMM 349 DNA, complete genome

Results provided by: BLAST nt database

BLAST nt - Assembly Identification - continued

Nucleotide Representa- tion	Description
742	CP010945 <i>Pseudomonas fluorescens</i> NCIMB 11764, complete genome
742	LT629760 <i>Pseudomonas trivialis</i> strain BS3111 genome assembly, chromosome: I
740	OV986001 <i>Pseudomonas fluorescens</i> SBW25 genome assembly, chromosome: 1
734	NG_021195 <i>Homo sapiens</i> CDK5 regulatory subunit associated protein 1 like 1 (CDKAL1), RefSeqGene on
733	CP022213 <i>Burkholderia gladioli</i> pv. <i>gladioli</i> strain FDAARGOS_188 chromosome 1, complete sequence
719	AC116614 <i>Homo sapiens</i> BAC clone CTD-2029L3 from 2, complete sequence
718	AM743169 <i>Stenotrophomonas maltophilia</i> K279a complete genome, strain K279a
698	CP089304 <i>Pseudomonas</i> sp. NIBR-H-19 chromosome, complete genome
662	AC060812 <i>Homo sapiens</i> chromosome 11, clone RP11-120E20, complete sequence
659	CP100603 <i>Pseudomonas fuscovaginae</i> UPB0736 chromosome, complete genome
649	AP023624 <i>Homo sapiens</i> DNA, sequence_id: unplaced_0139
642	CP049910 <i>Diaphorobacter</i> sp. HDW4A chromosome, complete genome
640	CP025263 <i>Pseudomonas</i> sp. S09G 359 chromosome
638	AC025568 <i>Homo sapiens</i> 12 BAC RP11-540D4 (Roswell Park Cancer Institute Human BAC Library) complete s
637	CP040439 <i>Stenotrophomonas maltophilia</i> strain PEG-141 chromosome, complete genome
637	CP019431 <i>Pseudomonas</i> sp. S35 chromosome, complete genome
636	AL021332 Human DNA sequence from clone RP3-398A12 on chromosome 6p23-25.1, complete sequence
620	CP049045 <i>Pseudomonas</i> sp. BIOMIG1BAC chromosome, complete genome
609	NG_028036 <i>Homo sapiens</i> protein tyrosine phosphatase non-receptor type 14 (PTPN14), RefSeqGene on ch
604	CP074409 <i>Pseudomonas syringae</i> strain KF529 chromosome, complete genome
594	AC016902 <i>Homo sapiens</i> BAC clone RP11-217B19 from 11, complete sequence
592	CP018420 <i>Pseudomonas veronii</i> strain R02, complete genome
592	AP023977 <i>Homo sapiens</i> DNA, sequence_id: unplaced_0492
590	CP039631 <i>Pseudomonas veronii</i> strain Pvy chromosome, complete genome
576	NG_016759 <i>Homo sapiens</i> kelch like family member 13 (KLHL13), RefSeqGene on chromosome X
576	AC091435 <i>Homo sapiens</i> chromosome 5 clone RP11-122C5, complete sequence
575	AC105001 <i>Homo sapiens</i> chromosome 8, clone CTD-2135J3, complete sequence
573	NG_054915 <i>Homo sapiens</i> pleckstrin homology and RhoGEF domain containing G4B (PLEKHG4B), RefSeqGene
573	AC097382 <i>Homo sapiens</i> BAC clone RP11-367J11 from 4, complete sequence
569	BX248407 Human DNA sequence from clone RP11-453B6 on chromosome 1, complete sequence
567	AL139275 Human DNA sequence from clone RP11-552E20 on chromosome 6p12.3-21.2, complete sequence
566	AC084871 <i>Homo sapiens</i> BAC clone RP11-701P16 from 4, complete sequence
565	AC140078 <i>Homo sapiens</i> 12 BAC RP13-7D7 (Roswell Park Cancer Institute Human BAC Library) complete seq
564	AC275605 <i>Homo sapiens</i> BAC clone CH17-120D21 from chromosome unknown, complete sequence
564	AC018719 <i>Homo sapiens</i> BAC clone RP11-573N21 from Xq23, complete sequence
561	AC007435 <i>Homo sapiens</i> , clone 6_C_10, complete sequence
561	AC006560 <i>Homo sapiens</i> 12 BAC RPC111-792F18 (Roswell Park Cancer Institute Human BAC Library) complet
558	CP077084 <i>Pseudomonas tritici</i> strain SWRI145 chromosome, complete genome
558	AC007464 <i>Homo sapiens</i> BAC clone RP11-542B5 from 2, complete sequence
557	AL683842 Human DNA sequence from clone RP11-47G11 on chromosome 10, complete sequence
555	CP003178 <i>Niastella koreensis</i> GR20-10, complete genome
554	CP034455 <i>Mesorhizobium</i> sp. M1A.F.Ca.IN.022.06.1.1 chromosome
553	AP019365 <i>Pseudomonas</i> sp. KU43P DNA, complete genome
553	CP029066 <i>Enterococcus mundtii</i> strain Pe103 chromosome, complete genome
551	CP044092 <i>Stenotrophomonas maltophilia</i> strain FDAARGOS_649 chromosome, complete genome
551	AC091608 <i>Homo sapiens</i> chromosome 1 clone RP11-97O14, complete sequence
550	LS483385 <i>Streptococcus sanguinis</i> strain NCTC7863 genome assembly, chromosome: 1
550	CP072333 <i>Porphyromonas</i> sp. oral taxon 275 strain W7780 chromosome, complete genome
548	CP116239 <i>Pseudomonas</i> sp. TUM22785 chromosome, complete genome
548	AC092111 <i>Homo sapiens</i> 12 BAC RP11-266K4 (Roswell Park Cancer Institute Human BAC Library) complete s
548	NG_012270 <i>Homo sapiens</i> potassium calcium-activated channel subfamily M alpha 1 (KCNMA1), RefSeqGene
547	AC010631 <i>Homo sapiens</i> chromosome 5 clone CTD-2282P23, complete sequence
545	AC107621 <i>Homo sapiens</i> chromosome 3 clone RP11-632N21, complete sequence
545	AC087244 <i>Homo sapiens</i> 12 BAC RP11-444N1 (Roswell Park Cancer Institute Human BAC Library) complete s

Results provided by: BLAST nt database

BLAST nt - Assembly Identification - continued

Nucleotide Representa- tion	Description
544	XR_007078591 PREDICTED: Homo sapiens uncharacterized LOC124906686 (LOC124906686), ncRNA
541	AL353802 Human DNA sequence from clone RP4-662P1 on chromosome 1p31.3-32.3, complete sequence
540	AL359475 Human DNA sequence from clone RP11-121P10 on chromosome 6, complete sequence
540	KR093655 Moraxella phage Mcat31, complete genome
538	CP047883 Streptococcus mitis strain S022-V3-A4 chromosome, complete genome
537	CP066057 Moraxella nonliquefaciens strain FDAARGOS_1006 chromosome, complete genome
535	AP024523 Streptococcus toyakuensis DNA, complete genome
535	AC073413 Homo sapiens BAC clone RP11-57B24 from 4, complete sequence
534	NG_051598 Homo sapiens phosphofructokinase, platelet (PFKP), RefSeqGene on chromosome 10; nuclear g
533	NG_016545 Homo sapiens BTB domain containing 9 (BTBD9), RefSeqGene on chromosome 6
532	AL136101 Human DNA sequence from clone RP5-954O23 on chromosome Xq22.2-23, complete sequence
531	AL356276 Human DNA sequence from clone RP11-367J7 on chromosome 1, complete sequence
530	BK049930 MAG TPA_asm: Caudoviricetes sp. isolate ct7mf1, partial genome
530	CP016207 Streptococcus sp. oral taxon 064 strain W10853 sequence
529	AL135785 Human DNA sequence from clone RP11-113O24 on chromosome 9p11-13.3, complete sequence
528	CP022202 Pseudomonas thivervalensis strain PLM3 genome
528	AL139110 Human DNA sequence from clone RP11-446J19 on chromosome Xq13.1-13.3, complete sequence
527	AC233295 Homo sapiens BAC clone RP11-751G7 from chromosome x, complete sequence
527	CP133298 Pseudomonas canadensis strain GZH03 chromosome, complete genome
526	NG_016478 Homo sapiens trafficking protein particle complex subunit 9 (TRAPPC9), RefSeqGene (LRG_1
524	NG_051023 Homo sapiens LDL receptor related protein 1B (LRP1B), RefSeqGene on chromosome 2
522	AF130342 Homo sapiens chromosome 8, complete sequence
520	AC078867 Homo sapiens 3 BAC RP11-605F14 (Roswell Park Cancer Institute Human BAC Library) complete s
519	DQ384492 Homo sapiens clone fa0622 genomic sequence
519	NG_183635 Homo sapiens ATAC-STARR-seq lymphoblastoid active region 3652 (LOC130004189) on chromosom
518	AC255503 Homo sapiens chromosome 20 clone 174779_ABC12_000046796400_O8, complete sequence
517	AC053527 Homo sapiens BAC clone RP11-692D12 from 4, complete sequence
516	NG_007092 Homo sapiens contactin associated protein 2 (CNTNAP2), RefSeqGene on chromosome 7
515	AB937783 Homo sapiens SAA2-SAA3 mRNA for SAA2-SAA3 isoform a, complete cds
515	AL138930 Human DNA sequence from clone RP11-528G1 on chromosome 1, complete sequence
515	AL357274 Human DNA sequence from clone RP11-685P13 on chromosome 6, complete sequence
514	CP017433 Achromobacter ruhlandii strain SCCH3:ACH 33-1365 genome
513	CP123067 Pseudomonas defluvi strain K4-sn1399 chromosome, complete genome
511	AC073352 Homo sapiens 3 BAC RP11-190C22 (Roswell Park Cancer Institute Human BAC Library) complete s
511	CP001721 Atopobium parvulum DSM 20469, complete genome
511	AC015819 Homo sapiens chromosome 18, clone RP11-405M12, complete sequence
510	AL356154 Human DNA sequence from clone RP11-102H24 on chromosome 10, complete sequence
510	AC009729 Homo sapiens 12 BAC RP11-1K3 (Roswell Park Cancer Institute Human BAC Library) complete seq
509	BK017231 MAG TPA_asm: Caudoviricetes sp. isolate ctWXE1, partial genome
505	NG_021246 Homo sapiens acyl-CoA wax alcohol acyltransferase 2 (AWAT2), RefSeqGene on chromosome X
505	AL731768 Human DNA sequence from clone RP13-324D24 on chromosome X, complete sequence
502	CP102283 Granulicatella adiacens ATCC 49175 chromosome, complete genome
502	AC237233 Homo sapiens FOSMID clone ABC16-1705E9 from chromosome 2, complete sequence
502	AC009731 Homo sapiens 12 BAC RP11-438N16 (Roswell Park Cancer Institute Human BAC Library) complete
501	CP040432 Stenotrophomonas maltophilia strain sm-RA9 chromosome, complete genome
500	AC018698 Homo sapiens BAC clone RP11-579C11 from 12, complete sequence
500	NG_032760 Homo sapiens growth arrest specific 1 (GAS1), RefSeqGene on chromosome 9
499	NG_016392 Homo sapiens MORC family CW-type zinc finger 4 (MORC4), RefSeqGene on chromosome X
499	AC060764 Homo sapiens chromosome 8, clone RP11-626A5, complete sequence
498	KR093656 Moraxella phage Mcat32, complete genome
498	CP089290 Candidatus Nanosynbacter sp. HMT-352 strain TM7-001 chromosome
498	NG_029510 Homo sapiens protein tyrosine kinase 2 beta (PTK2B), RefSeqGene on chromosome 8
497	CP045916 Pseudomonas aeruginosa strain CF39S chromosome, complete genome
497	AK123450 Homo sapiens cDNA FLJ41456 fis, clone BRSTN2012320

Results provided by: BLAST nt database

BLAST nt - Assembly Identification - continued

Nucleotide Representa- tion	Description
496	AC119044 Homo sapiens 12 BAC RP11-23J18 (Roswell Park Cancer Institute Human BAC Library) complete s
495	CP075820 Pseudomonas aeruginosa strain PaLo36 chromosome, complete genome
495	CP046308 Mycobacterium tuberculosis strain FDAARGOS_751 chromosome, complete genome
492	CP048071 Mycobacterium tuberculosis strain RW-TB008 chromosome, complete genome
492	CP016844 Carnobacterium maltaromaticum strain TMW 2.1581 chromosome, complete genome
492	CP117429 Pseudomonas simiae strain FP689 chromosome, complete genome
492	AC073587 Homo sapiens chromosome 10 clone RP11-572P18, complete sequence
491	AC025470 Homo sapiens chromosome 5 clone CTD-2516K3, complete sequence
489	MG660520 Homo sapiens isolate Chlk1727 haplogroup D5a2a1-161721 mitochondrion, complete genome
488	AC012150 Homo sapiens 12 BAC RP11-946L16 (Roswell Park Cancer Institute Human BAC Library) complete
488	CP069362 Marinitoga sp. BP5-C20A chromosome, complete genome
488	AC092033 Homo sapiens BAC clone RP11-794I22 from 7, complete sequence
487	AL392173 Human DNA sequence from clone RP11-158M9 on chromosome Xq26.1-27.1, complete sequence
485	AL022344 Human DNA sequence from clone Y214H10 on chromosome 10, complete sequence
485	LS483383 Streptococcus cristatus strain NCTC12479 genome assembly, chromosome: 1
484	NG_008477 Homo sapiens SURF1 cytochrome c oxidase assembly factor (SURF1), RefSeqGene on chromosome
483	AC090669 Homo sapiens 12 BAC RP11-780K2 (Roswell Park Cancer Institute Human BAC Library) complete s
483	CP117461 Pseudomonas sp. FP1740 chromosome, complete genome
482	CP067992 Streptococcus mitis strain S022-V7-A3 chromosome, complete genome
482	AC090821 Homo sapiens chromosome 8, clone CTD-2309H9, complete sequence
480	NG_005510 Homo sapiens ENTR1 pseudogene 1 (ENTR1P1) on chromosome 18
480	CP014326 Streptococcus mitis strain SVGS_061 chromosome, complete genome
479	CP025599 Mycobacterium tuberculosis strain GG-45-11 chromosome, complete genome
478	NG_013260 Homo sapiens SAM and SH3 domain containing 3 (SASH3), RefSeqGene on chromosome X
478	NM_020710 Homo sapiens leucine rich repeat containing 47 (LRRC47), mRNA
477	NG_009409 Homo sapiens DLG associated protein 2 (DLGAP2), RefSeqGene on chromosome 8
476	AC004840 Homo sapiens PAC clone RP4-607J2 from 7, complete sequence
476	AC009275 Homo sapiens chromosome 7 clone RP11-38M8, complete sequence
475	CP027753 Pseudomonas chlororaphis strain B25 chromosome, complete genome
475	AC279591 Homo sapiens chromosome unknown clone VMRC59-384G24, complete sequence
474	AL353756 Human DNA sequence from clone RP11-415D9 on chromosome 9, complete sequence
474	AC279687 Homo sapiens chromosome unknown clone VMRC59-495H23, complete sequence
473	NG_011681 Homo sapiens DISC1 scaffold protein (DISC1), RefSeqGene on chromosome 1
473	NG_050926 Homo sapiens microtubule actin crosslinking factor 1 (MACF1), RefSeqGene on chromosome 1
472	AL157404 Human DNA sequence from clone RP1-148L21 on chromosome 1q21.2-22, complete sequence
472	XR_007073811 PREDICTED: Homo sapiens uncharacterized LOC107986129 (LOC107986129), transcript varian
470	NG_016711 Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), RefSeqGene (LRG_1127) on chrom
469	AL591521 Human DNA sequence from clone RP5-965F6 on chromosome 1, complete sequence
469	NG_008493 Homo sapiens estrogen receptor 1 (ESR1), RefSeqGene (LRG_992) on chromosome 6
469	AC243971 Homo sapiens BAC clone CH17-437O13 from chromosome 1, complete sequence
467	XR_007071590 PREDICTED: Homo sapiens uncharacterized LOC107985903 (LOC107985903), ncRNA
465	AL356417 Human DNA sequence from clone RP11-13P5 on chromosome 6, complete sequence
464	LT599583 Pseudomonas veronii 1YdBTEX2 genome assembly, chromosome: PVE_r1
464	AL138762 Human DNA sequence from clone RP11-179B2 on chromosome 10, complete sequence
464	AC087311 Homo sapiens 12 BAC RP11-267D19 (Roswell Park Cancer Institute Human BAC Library) complete
464	NG_051298 Homo sapiens sidekick cell adhesion molecule 1 (SDK1), RefSeqGene on chromosome 7
463	AP023478 Homo sapiens DNA, chromosome 18, nearly complete genome
463	XM_054336437 PREDICTED: Homo sapiens potassium voltage-gated channel subfamily C member 4 (KCNC4),
462	AP017423 Pseudomonas izuensis DNA, complete genome
462	AL365274 Human DNA sequence from clone RP11-298A17 on chromosome 9, complete sequence
460	CP102248 Stenotrophomonas sp. CD2 chromosome, complete genome
460	CP034664 Moraxella catarrhalis strain 74P50B1 chromosome, complete genome
460	AC012506 Homo sapiens BAC clone RP11-498O22 from 2, complete sequence
459	MK617255 Homo sapiens isolate 237_Sb haplogroup J1c5 mitochondrion, complete genome

Results provided by: BLAST nt database

BLAST nt - Assembly Identification - continued

Nucleotide Representa- tion	Description
459	AC093662 Homo sapiens BAC clone RP11-477A19 from 7, complete sequence
458	AL365500 Human DNA sequence from clone RP11-232C13 on chromosome 10, complete sequence
458	AP002008 Homo sapiens genomic DNA, chromosome 11q clone:RP11-794P6, complete sequences
457	CP072524 Neisseria sicca strain NS20201025 chromosome, complete genome
456	AC277733 Homo sapiens chromosome 2 clone VMRC62-168C17, complete sequence
455	CP040438 Stenotrophomonas maltophilia strain PEG-173 chromosome, complete genome
455	XM_054362760 PREDICTED: Homo sapiens golgin A1 (GOLGA1), transcript variant X4, mRNA
454	KR093629 Moraxella phage Mcat5, complete genome
454	AC034214 Homo sapiens chromosome 5 clone CTD-2001E22, complete sequence
453	AC211860 Homo sapiens FOSMID clone ABC12-47035100O10 from chromosome 12, complete sequence
453	CP060529 Pseudomonas putida strain GIMC5401:PPKH-115 chromosome
452	AC007030 Homo sapiens PAC clone RP5-1112I4 from 7, complete sequence
451	AL022067 Human DNA sequence from clone RP1-134E15 on chromosome 6q21, complete sequence
451	CP128647 Mogibacterium neglectum strain ATCC 700924 chromosome, complete genome
451	AC092058 Homo sapiens chromosome 3 clone RP11-667E17, complete sequence
451	AP002346 Homo sapiens genomic DNA, chromosome 11q clone:CTD-2387M17, complete sequences
450	CP087198 Pseudomonas sp. B21-010 chromosome, complete genome
449	NG_021375 Homo sapiens discs large MAGUK scaffold protein 2 (DLG2), RefSeqGene on chromosome 11; nu
449	CP013997 Pseudomonas monteilii strain USDA-ARS-USMARC-56711 chromosome, complete genome
448	CP087170 Pseudomonas rhodesiae strain B21-046 chromosome, complete genome
448	NG_046798 Homo sapiens family with sequence similarity 183 member E, pseudogene (FAM183EP) on chrom
447	AC117452 Homo sapiens 3 BAC RP11-341J3 (Roswell Park Cancer Institute Human BAC Library) complete se
447	NG_012324 Homo sapiens keratin 80 (KRT80), RefSeqGene on chromosome 12
446	MF696106 Homo sapiens isolate COM18 mitochondrion, complete genome
446	NG_008983 Homo sapiens 5'-aminolevulinat synthase 2 (ALAS2), RefSeqGene (LRG_1163) on chromosome
446	AC079148 Homo sapiens BAC clone RP11-111J6 from 2, complete sequence
445	CP106751 Granulicatella adiacens strain KHUD_009 chromosome, complete genome
445	AP023481 Homo sapiens DNA, chromosome 21, nearly complete genome
444	AL512884 Human DNA sequence from clone RP13-775K13 on chromosome Xp11.1-11.22, complete sequence
441	AC006499 Homo sapiens chromosome 4 clone C0494H11, complete sequence
440	KX353852 Pseudomonas fragi strain A22 plasmid pPFL, complete sequence
440	AC104331 Homo sapiens chromosome 3 clone RP11-543A18, complete sequence
440	AC009970 Homo sapiens BAC clone RP11-440P5 from 2, complete sequence
440	NG_047074 Homo sapiens regulatory factor X4 (RFX4), RefSeqGene on chromosome 12
439	AC120305 Homo sapiens 3 BAC RP11-570H17 (Roswell Park Cancer Institute Human BAC Library) complete s
439	LS483433 Pseudomonas mucidolens strain NCTC8068 genome assembly, chromosome: 1
439	GQ154676 Homo sapiens isolate 41354s Fc fragment of IgG low affinity IIIa receptor precursor (FCGR3A
438	CP079822 Rothia mucilaginosa strain LPB0405 chromosome, complete genome
438	AC020894 Homo sapiens chromosome 5 clone CTC-293A9, complete sequence
438	CP023510 Rothia mucilaginosa strain FDAARGOS_369 chromosome, complete genome
438	CP052863 Stenotrophomonas maltophilia strain CF13 chromosome, complete genome
437	CP015600 Pseudomonas antarctica strain PAMC 27494, complete genome
437	AC022425 Homo sapiens chromosome 1 clone CTD-2302K4, complete sequence
436	AC017006 Homo sapiens BAC clone RP11-110G2 from 2, complete sequence
436	AC277842 Homo sapiens chromosome 6 clone CH17-58K5, complete sequence
436	BK041139 MAG TPA_asm: Bacteriophage sp. isolate ctpxo11, partial genome
436	AC079804 Homo sapiens BAC clone RP11-740N7 from 7, complete sequence
436	AP023803 Homo sapiens DNA, sequence_id: unplaced_0318
436	AL008626 Human DNA sequence from clone RP5-1114G22 on chromosome 1q24-25, complete sequence
435	AC099566 Homo sapiens chromosome 1 clone RP4-798D13, complete sequence
435	AC022681 Homo sapiens chromosome 8, clone RP11-731D24, complete sequence
434	AC079612 Homo sapiens BAC clone RP11-314A6 from 2, complete sequence
434	XR_007083106 PREDICTED: Homo sapiens uncharacterized LOC124903028 (LOC124903028), transcript varian
434	CP089288 Candidatus Nanosynbacter sp. HMT-352 strain TM7-037 chromosome

Results provided by: BLAST nt database

BLAST nt - Assembly Identification - continued

Nucleotide Representa- tion	Description
433	CP065997 Achromobacter deleyi strain FDAARGOS_1050 chromosome, complete genome
433	AC243898 Homo sapiens BAC clone CH17-116H17 from chromosome 1, complete sequence
432	CP011117 Pseudomonas synxantha strain LBUM223 chromosome, complete genome
432	CP035368 Haemophilus parainfluenzae strain LC_1315_18 chromosome, complete genome
432	CP032620 Streptococcus koreensis strain JS71 chromosome, complete genome
432	AC275880 Homo sapiens chromosome 11 clone VMRC64-116P20, complete sequence
431	CP027762 Pseudomonas sp. LBUM920 chromosome, complete genome
431	CP068257 Homo sapiens isolate CHM13 chromosome 21
431	NG_047029 Homo sapiens catenin alpha 1 (CTNNA1), RefSeqGene on chromosome 5
431	CP061536 Rothia mucilaginosa strain CECT30005 chromosome
431	AC275236 Homo sapiens chromosome 2 clone CH17-116P13, complete sequence
430	CP076562 Eubacterium sp. MSJ-33 chromosome, complete genome
429	CP034442 Streptococcus oralis subsp. dentisani strain F0392 chromosome, complete genome
322	CP130775 Mycobacterium tuberculosis strain MTb-Oman-3214121 chromosome, complete genome
251	AP017901 Mycobacterium tuberculosis DNA, complete genome, strain: NCGM946K2
165	CP019610 Mycobacterium tuberculosis strain H54 chromosome, complete genome
141	CP046309 Mycobacterium tuberculosis strain FDAARGOS_750 chromosome, complete genome

Results provided by: BLAST nt database

Report Description

Input to create this report was either FASTA, or single/paired FASTQ/s.

If built from FASTA, contigs have been identified using Kraken2/Bracken; and assembly metrics, expected genome size compared against total assembly length, MLST, PlasmidFinder, AMRFinderPlus and BLAST results have been reported. In addition to these tests, if report was built from FASTQ/s, sequence technology, FASTQ metrics and coverage graph against the top BLAST hit was also reported. Finally, if Kraken2/Bracken top finding was Salmonella SeqSero2 and CRISPR SeroSeq additionally reported. See table below for summary of tests reported.

Expected results are approximately based on a 4,500,000 base bacterial genome.

When tests are run and there are no significant findings the test's banner and a "no results" message will still be included in this report. If this is not seen, yet test is expected, the report is invalid.

	FASTA	FASTQ	FASTQ Identified as Salmonella
Sequence Technology		X	X
FASTQ metrics		X	X
Kraken2/Bracken	X	X	X
Assembly metrics	X	X	X
Expected Genome Size	X	X	X
MLST	X	X	X
PlasmidFinder	X	X	X
AMRFinderPlus	X	X	X
Coverage Graph		X	X
BLAST	X	X	X
SeqSero2			X
CRISPR SeroSeq			X

Table 1: Test Summary

Sequence Technology

Single FASTQ is assumed to have been generated from Ion S5 System using S5 chemistry. Paired reads are assumed to have been generated from Illumina MiSeq System. Read length is reported based on average read length and rounded up to 50th number.

FASTQ metrics

Filename: Input files

File Size: Compressed input file size (.gz). *Expected: >150MB*

Q30 Passing: Percentage of reads with an average Phred score above 30. *Expected: >70%*

Mean Read Score: Average Phred score of all base calls. *Expected: >30*

Kraken2/Bracken

Bracken computes specie abundance using Kraken2 taxonomy labels. Fraction of reads are reported only when greater than 1% of total reads.

Kraken2 database was built from the following:

Libraries:

archaea: RefSeq complete archaeal genomes
 bacteria: RefSeq complete bacterial genomes
 plasmid: RefSeq plasmid nucleotide/protein sequences
 viral: RefSeq complete viral genomes
 human: GRCh38 human genome
 fungi: RefSeq complete fungal genomes
 plant: RefSeq complete plant genomes
 protozoa: RefSeq complete protozoan genomes
 UniVec Core: A subset of UniVec chosen to minimize false positive hits to the vector database

Custom genomes:

Bos taurus (cow)
 Sus scrofa (pig)
 gallus gallus (chicken)
 Odocoileus virginianus (white-tailed deer)
 Panthera tigris altaica (tiger)
 Felis catus (house cat)
 Canis lupus familiaris (dog)
 Loxodonta africana (elephant)
 Tursiops truncatus (bottlenose dolphin)
 Anas platyrhynchos (mallard)
 Cyprinus carpio (common carp)
 Nanorana parkeri (frog)
 Aedes albopictus (mosquito)

Unclassified reads were either poor quality or no perfect sample k-mers ($k=35$) mapped to read sequence from the Kraken2 database build.

Assembly metrics

Reads are assembled using SPAdes when FASTQs are used to generate report. When a FASTA is used SPAdes is assumed assembler.

Metrics can vary greatly. Numbers outside expected values should not always be interpreted as a poor sample, but should be considered against other test results.

Scaffolds: Total contig count of assembly. *Expected: <300*

Total Length: Total length of all sequences. *Expected: 4,500,000*

Longest Scaffold: Longest assembled sequence. *Expected: >200,000*

Scaffolds >1K nt: Sequences greater than 1,000 nucleotides in length. *Expected: >200*

N50: Half of the total assembled length is made from sequence greater than this value. *Expected: >100,000*

Mean Read Depth: Estimated average read depth across total assembly length. *Expected: >50X*

Genome Size Comparisons

Expected genome size is found using top Bracken identification. The genome size is estimated by providing the species name to NCBI which returns the expected size. If NCBI does not return a genome size for the top Bracken identification the Bracken list is iterated from highest to lowest read identification until genome size is found. If an expected genome size is still not found a value of 5,000,000 is used.

The comparison between sample assembly size and expected genome size is very important when determining contamination and genome completeness.

MLST

Assembly file scanned for PubMLST typing schemes using MLST tool.

Schema-Sequence type: Traditional PubMLST typing scheme found

MLST Detail: Gene and allele IDs, see link for explanations for "n", "~", "?", "-" and "n, m" notation.

PlasmidFinder

PlasmidFinder tool used to target plasmids.

Description: NCBI accession number and identification

Length: Sequence length of described accession

Contig ID: Assembly identification of found plasmid

HSP Length: High score pairs length of BLAST database sequence identifying plasmid

% Identity: Percentage of HSP bases similar to matched findings

% Coverage: Percentage of HSP bases aligning to matched findings

AMRFinderPlus

AMRFinderPlus finds acquired antimicrobial resistance genes in assembled nucleotide sequences and resistance-associated point mutations in select taxa. Gene classes found include AMR, point mutations, virulence factors, biocide, heat, acid, and metal resistance genes.

This report includes providing an organism option to AMRFinderPlus if Bracken identification fits select options. When an organism option is provided point mutations are screened and some common findings are suppressed.

AMRFinderPlus Organism Option: Option used to get organism-specific results

Contig ID: Assembly identification of found element

Element: Classification of the AMRFinderPlus gene

Gene: AMR gene

Name: Gene detail

% Cov: Percentage of protein aligning to matched findings

% Similar: Percentage of protein similar to matched findings

Coverage Graph

Reads aligned using BWA to the top BLAST accession hit. When greater than 100X depth-of-coverage log read depth is graphed. If less than 100X a linear read depth is graphed.

ID: NCBI accession aligned against

Average Depth: Average depth-of-coverage across sequence aligned against

Genome Length: Length of genome aligned against

Ambiguous SNPs: Ambiguous SNP count. A high count can indicate poor WGS (i.e. low coverage), a multiple-strain sample or contamination with a closely related strain.

ID Detail: Accession detail

BLAST

Assembly BLAST against nt database. Totaled nucleotide representation identified as top hit.

Nucleotide Representation: Summed contig lengths based on same accession top hit identifications.

Description: NCBI accession number and identification

SeqSero2

SeqSero2 targets the O (wzx and wzy genes) and H (fliC and fljB genes) antigens to determine serotype. When more than one O antigen, or two or more H antigens are found it can indicate the presence of contamination.

Predicted serotype(s): Predicted serotype based on O and H antigens

Predicted antigenic profiles: Shorthand profiles

Predicted subspecies: Predicted subspecies if available

Note: Special notes from SeqSero when provided

Bottom: Contig detail of SeqSero findings